STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/520,033_
Source: _PCT/10_
Date Processed by STIC: _1/10/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *10/520,033*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
    prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
    Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped

    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
    (NEW RULES)   <210> sequence id number
    <400> sequence id number
    000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide;</u> "Xaa" can **only** represent a single <u>amino acid</u>

PCT

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw   *see item 2 on Error Summary Sheet*

```
      3 <110> APPLICANT: Chan, Raquel
      5 <120> TITLE OF INVENTION: Transcription factor gene induced by water deficit
conditions and
      6       abscisic acid from Helianthus annuus, promoter and transgenic plants
      8 <130> FILE REFERENCE: US PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/520,033
C--> 10 <141> CURRENT FILING DATE: 2004-12-30
     10 <160> NUMBER OF SEQ ID NOS: 22
     12 <170> SOFTWARE: PatentIn version 3.1
```

these lines exceed 72 characters

see pp 1-6

ERRORED SEQUENCES   *delete all alphabetical headings*   *Does Not Comply*
                                                             Corrected Diskette Needed

```
E--> 14 <210>         SEQ ID NO.1     1 <- just show "1"
     15 <211> LENGTH: 774
     16 <212> TYPE: DNA
     17 <213> ORGANISM: Helianthus annuus
     19 <400> SEQUENCE: 1
```

do NOT use alphabetical headings in a "new" sequence. Rules format sequence listing

```
     20 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg    60
     22 tctcttcaac aagtacccac aacagaaaca accaccagga agaaccgaaa cgaggggcgg   120
     24 aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga   180
     26 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg   240
     28 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat   300
     30 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag   360
     32 aatcaggccc tactcaatca ggtatggttg caaacttaca atgttgcatt caactattta   420
     34 agtagttttg aatttttgtg acaataaaga ttgacaaatg ttgtttgata attgattaac   480
     36 agttggaggt gctgagaaat gtagcagaaa agcatcaaga gaaaactagt agtagtggca   540
     38 gcggtgaaga atcggatgat cggtttacga actctccgga cgttatgttt ggtcaagaaa   600
     40 tgaatgttcc gtttttgcgac ggttttgcgt actttgaaga aggaaacagt ttgttggaga   660
     42 ttgaagaaca actgccagac cctcaaaagt ggtgggagtt ctaaagagta aagaaggatg   720
     44 tagaagtagt agagtaaaaa ctaaaacata ccagatagtt ggtttacact ttgt          774
E--> 47 <210>            SEQ ID NO 2
     48 <211> LENGTH: 673
     49 <212> TYPE: DNA
     50 <213> ORGANISM: Helianthus annuus
     52 <400> SEQUENCE: 2
     53 tcactagtac cataatattc acaaacacac acacctcaga aacgaagctt gcacataatg    60
     55 tctcttcaac aagtacccac aacagaaaca accaccagga agaaccgaaa cgaggggcgg   120
     57 aaacgattta ccgacaaaca aataagtttc ctagagtaca tgtttgagac acagtcgaga   180
     59 cccgagttaa ggatgaaaca ccagttggca cataaactcg ggcttcatcc tcgtcaagtg   240
     61 gcgatatggt tccagaacaa acgcgcgcga tcaaagtcga ggcagattga gcaagagtat   300
     63 aacgcgctaa agcataacta cgagacgctt gcgtctaaat ccgagtctct aaagaaagag   360
     65 aatcaggccc tactcaatca ggtggaggtg ctgagaaatg tagcagaaaa gcatcaagag   420
     67 aaaactagta gtagtggcag cggtgaagaa tcggatgatc ggtttacgaa ctctccggac   480
```

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

```
    69 gttatgtttg gtcaagaaat gaatgttccg ttttgcgacg gttttgcgta ctttgaagaa    540
    71 ggaaacagtt tgttggagat tgaagaacaa ctgccagacc ctcaaaagtg gtgggagttc    600
    73 taaagagtaa agaaggatgt agaagtagta gagtaaaaac taaaacatac cagatagttg    660
    75 gtttacactt tgt                                                         673
E--> 78 <210>        SEQ ID NO 3
    79 <211> LENGTH: 1221
    80 <212> TYPE: DNA
    81 <213> ORGANISM: Helianthus annuus
    83 <220> FEATURE:
    84 <221> NAME/KEY: promoter
    85 <222> LOCATION: (1)..(1221)
    86 <223> OTHER INFORMATION: Large allele
 89 <400> SEQUENCE: 3
    90 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca     60
    92 caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc    120
    94 atattaaaag tagtagcccc cacccccatt tgttacctac catttcccac tttaataatc    180
    96 acccacgcta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa    240
    98 ccaaattttt tttagtggaa aacaaattcc ccaaatagaa tactaacgaa attcatcgca    300
   100 tcagaataca ctcatctctg aacagtggcg aagcttgacg ttttcgacgg ggggtcggaa    360
   102 aacgtatgta cccgaaattt ctatagaatc ggggggtcga aaacgtatat acccaaaatt    420
   104 tctatacgaa aactacatat ataacactac tgagcaaaaa gttcgggggt tcgggcgccc    480
   106 ctcccggccc cttcaaagct tcgccaatgt ctctgaaccg aagaaaaccc tcactcgtct    540
   108 actagccaat gaatcctcac cagggaaacc ctcactcgtc ttactggact attggcgctt    600
   110 ccaaatggac tacttgcgaa attcaccaca tcgggataca ctcgtctact gcggtgaggt    660
   112 aaaacccgct tggctcaagg atcgaactag cgattgctgc ctactcgcct aatctcccat    720
   114 catcaacagg tgccgccgaa acaaaatgct gggggcggga gttgaaccta ggtccagtga    780
   116 cgcacccatg aatttttttt ctagggatgc gaacgagtgg tttaaccata cttttaagag    840
   118 gtgcgatcgg aaattttacc tataaaatac actaaaaaag ttccaagggt ccacccaccc    900
   120 cttaacctaa gtccgccttt gtctggatca cgtgaaacat caggtctctc ccttaccagt    960
   122 ccagctacga ctcattgaca aaatatcaaa accatatgat tttgagtttt atctcaaccg   1020
   124 aaagtgacat catgacagag aatcgacata accaaaacgt gtaaacgtac aactcaccat   1080
   126 tgcgttgaaa aggacaaaac aggtaggatt cttgtcaaat tcaacgcgta cacctgtgct   1140
   128 tcatctaaac cccatacttt aagaacctttt ataaagacca ctcactatat atacacatat   1200
   130 ataatatcac ttatcaaacc c                                              1221
E--> 133 <210>        SEQ ID NO 4
   134 <211> LENGTH: 28
   135 <212> TYPE: DNA
   136 <213> ORGANISM: Artificial
   138 <220> FEATURE:
   139 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Hind I
   140       II site
 142 <400> SEQUENCE: 4
   143 gcgaagcttg atgcgaacga gtggttta                                        28
E--> 146 <210>        SEQ ID NO 5
   147 <211> LENGTH: 28
   148 <212> TYPE: DNA
   149 <213> ORGANISM: Artificial
   151 <220> FEATURE:
   152 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Sal I
```

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\01102006\J520033.raw

```
    153         site
    155 <400> SEQUENCE: 5
    156 gcggtcgaca cctggcacat cgtatctt                                    28
E--> 159 <210> :        SEQ ID NO. 6
    160 <211> LENGTH: 27
    161 <212> TYPE: DNA
    162 <213> ORGANISM: Artificial
    164 <220> FEATURE:
    165 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Bam HI
    166         site
    168 <400> SEQUENCE: 6
    169 cgcggatccg agggtttgat aagtgat                                     27
E--> 172 <210>         SEQ ID NO. 7
    173 <211> LENGTH: 27
    174 <212> TYPE: DNA
    175 <213> ORGANISM: Artificial
    177 <220> FEATURE:
    178 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Hind I
    179         II site
    181 <400> SEQUENCE: 7
    182 cccaagctta acctaagtcc gcctttg                                     27
E--> 185 <210>         SEQ ID NO. 8
    186 <211> LENGTH: 27
    187 <212> TYPE: DNA
    188 <213> ORGANISM: Artificial
    190 <220> FEATURE:
    191 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Hind II
    192         I site
    194 <400> SEQUENCE: 8
    195 ggcaagctta tctcaaccga aagtgac                                     27
E--> 198 <210>         SEQ ID NO. 9
    199 <211> LENGTH: 19
    200 <212> TYPE: DNA
    201 <213> ORGANISM: Artificial
    203 <220> FEATURE:
    204 <223> OTHER INFORMATION: Designed oligonucleotide based on the 5' promoter
    206 <400> SEQUENCE: 9
    207 atttcgcaag tagtccatt                                              19
E--> 210 <210>         SEQ ID NO. 10
    211 <211> LENGTH: 1015
    212 <212> TYPE: DNA
    213 <213> ORGANISM: Helianthus annuus
    215 <400> SEQUENCE: 10
    216 gatccaattg gaccacctgg cacatcgtat cttatctctt ttgtcgtttc caacacacca   60
    218 caacacacct acaaacgtgt caattcacac ttcaccaatt tcatttcctt ttagtcaatc  120
    220 atattaaaag tagtagcccc cacccccatt tgttacctac catttcccac tttaataatc  180
    222 acccacgcta tgtccacttg tacttttgtt tgcacacaac tcttcccata aaatatcaaa  240
    224 ccaaattttt tttaatggaa aacaaatact tcaaatgcac tattggtgaa attcaccaca  300
    226 tcagaataca cccgtctcta ctcatctact ggccaacgaa tcttcacggg ggaaaccctc  360
```

```
    228 actcgtctac tgggactact ggcgcttcaa aatggactac tgacaaaatt caccacatcg     420
    230 ggatacactt gtctactgcg gtgaggtaaa atccgccgct cagctcaatg atcgaactag     480
    232 cgatcgccac ccactcacct tgtctcccat catcaccagg tgccgccaaa acaaaatgtt     540
    234 gggggcggga attgaaccta ggtccagtgg cgcacccatg aatttttttt ctagggatgc     600
    236 gaacgagtga tttaaccata cttttaagag gtgcgatcgg aaattttacc tataaaatat     660
    238 actaaaaaaa tttcaagggt ccgcccaccc accccttaac ctaagtccgc ctctgcctgg     720
    240 atcacgtgaa acatcaggtc tctctcttac cagttcacct acaactcatt gacaaaatat     780
    242 caaaaccata tgattttgag ttttatctca accgaaagtg acatcatgac agagaatcga     840
    244 cataaccaaa acgtgtaaac gtacaactca ccattgcgtt gaaaaggaca aaacaggtag     900
    246 gattcttgtc aaattcaacg cgtacacctg tgcttcatct aaaccccata ctttaagaac     960
    248 ctttataaag accactcact atatatacac atatataata tcacttatca aaccc         1015
E--> 251 <210>          SEQ ID NO. 11
    252 <211> LENGTH: 28
    253 <212> TYPE: DNA
    254 <213> ORGANISM: Artificial
    256 <220> FEATURE:
    257 <223> OTHER INFORMATION: Designed oligonucleotide that matches nucleotides 81-100 of
the H
    258        ahb-4 cDNA sequence and having Bam HI site
E--> 260 <400> SEQUENCE: 11
    261 ggcggatcca acagaaacaa ccaccagg                                          28
E--> 264 <210>          SEQ ID NO. 12
    265 <211> LENGTH: 29
    266 <212> TYPE: DNA
    267 <213> ORGANISM: Artificial
    269 <220> FEATURE:
    270 <223> OTHER INFORMATION: Designed oligonucleotide for cloning 5' cDNA and having Bam
HI s
    271        ite
E--> 273 <400> SEQUENCE: 12
    274 ggcggatccc ctgqtggttg tttctgttg                                         29
E--> 277 <210>          SEQ ID NO. 13
    278 <211> LENGTH: 34
    279 <212> TYPE: DNA
    280 <213> ORGANISM: Artificial
    282 <220> FEATURE:
    283 <223> OTHER INFORMATION: oligonucleotide based on 5' cDNA and having Xho I site
E--> 285 <400> SEQUENCE: 13
    286 gaggactcga gctcaagttt tttttttttt tttt                                   34
E--> 289 <210>          SEQ ID NO. 14
    290 <211> LENGTH: 18
    291 <212> TYPE: DNA
    292 <213> ORGANISM: Artificial
    294 <220> FEATURE:
    295 <223> OTHER INFORMATION: Oligonucleotide based on 5' cDNA and having Xho I site
E--> 297 <400> SEQUENCE: 14
    298 gaggactcga gctcaagc                                                     18
E--> 301 <210>          SEQ ID NO. 15
    302 <211> LENGTH: 29
    303 <212> TYPE: DNA
    304 <213> ORGANISM: Artificial
```

```
    306 <220> FEATURE:
    307 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter and having
Eco RI
    308      site
    310 <400> SEQUENCE: 15
    311 gccgaattca gattgagcaa gagtataac                            29
E--> 314 <210>            SEQ ID NO.16
    315 <211> LENGTH: 19
    316 <212> TYPE: DNA
    317 <213> ORGANISM: Artificial
    319 <220> FEATURE:
    320 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
    322 <400> SEQUENCE: 16
    323 acctttataa agaccactc                                       19
E--> 326 <210>            SEQ ID NO.17
    327 <211> LENGTH: 19
    328 <212> TYPE: DNA
    329 <213> ORGANISM: Artificial
    331 <220> FEATURE:
    332 <223> OTHER INFORMATION: Designed oligonucleotide based on the promoter
    334 <400> SEQUENCE: 17
    335 acgcaatggt gaqttgtac                                       19
E--> 338 <210>            SEQ ID NO.18
    339 <211> LENGTH: 24
    340 <212> TYPE: DNA
    341 <213> ORGANISM: Artificial
    343 <220> FEATURE:
    344 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
    346 <400> SEQUENCE: 18
    347 aattcagatc tcaataattg agag                                 24
E--> 350 <210>            SEQ ID NO.19
    351 <211> LENGTH: 24
    352 <212> TYPE: DNA
    353 <213> ORGANISM: Artificial
    355 <220> FEATURE:
    356 <223> OTHER INFORMATION: oligonucleotide to DNA-binding assays
    358 <400> SEQUENCE: 19
    359 gatcctctca attattgaga tctg                                 24
E--> 362 <210>            SEQ ID NO.20
    363 <211> LENGTH: 30
    364 <212> TYPE: DNA
    365 <213> ORGANISM: Artificial
    367 <220> FEATURE:
    368 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
    370 <400> SEQUENCE: 20
    371 gcgggatcca ccatgtctct tcaacaagta                           30
E--> 374 <210>            SEQ ID NO.21
    375 <211> LENGTH: 30
    376 <212> TYPE: DNA
    377 <213> ORGANISM: Artificial
```

RAW SEQUENCE LISTING   DATE: 01/10/2006
PATENT APPLICATION: US/10/520,033   TIME: 08:16:21

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\01102006\J520033.raw**

```
379 <220> FEATURE:
380 <223> OTHER INFORMATION: Oligonucleotide having Sac I site
382 <400> SEQUENCE: 21
383 gccgagctct tagaactcca accacttttg                                    30
386 <210>            SEQ ID NO.22
387 <211> LENGTH: 27
388 <212> TYPE: DNA
389 <213> ORGANISM: Artificial
391 <220> FEATURE:
392 <223> OTHER INFORMATION: Oligonucleotide having Bam HI site
394 <400> SEQUENCE: 22
395 ggcggatccg tctcccagtt gttcttc                                       27
398 7
```

delete

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
L:47 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:52 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2
L:78 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:89 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3
L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:142 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
L:146 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:155 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5
L:159 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:168 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6
L:172 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:181 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
L:185 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:194 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8
L:198 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:206 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9
L:210 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:215 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10
L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:260 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11
L:264 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:273 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12
L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:285 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13
L:289 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:297 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14
L:301 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15
L:314 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:322 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16
L:326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:334 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17
L:338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:346 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18
L:350 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:358 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19
L:362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:370 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20
L:374 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21
L:386 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:394 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22
L:398 M:254 E: No. of Bases conflict, this line has no nucleotides.
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